ETC 2420/5242 Lab 4 2017

SOLUTION

Week 4

Purpose

This lab is to examine different statistical distributions, fit distributions to samples by estimating the parameters by maximum likelihood and checking the fit with QQ-plots.

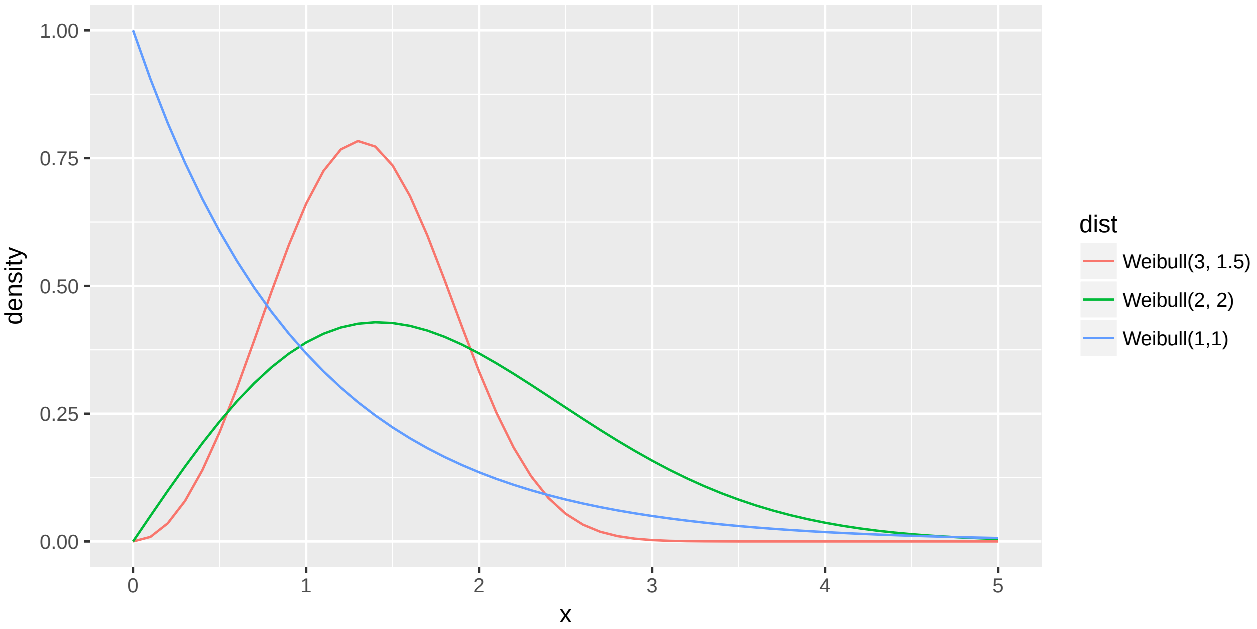
Reading

Read the material on maximum likelihood estimation at https://onlinecourses.science.psu.edu/stat414/node/191.

Read the code in the lecture notes from Week 3. Particularly look at the functions for making QQ-plots, computing and plotting the likelihood functions.

Warmup exercises

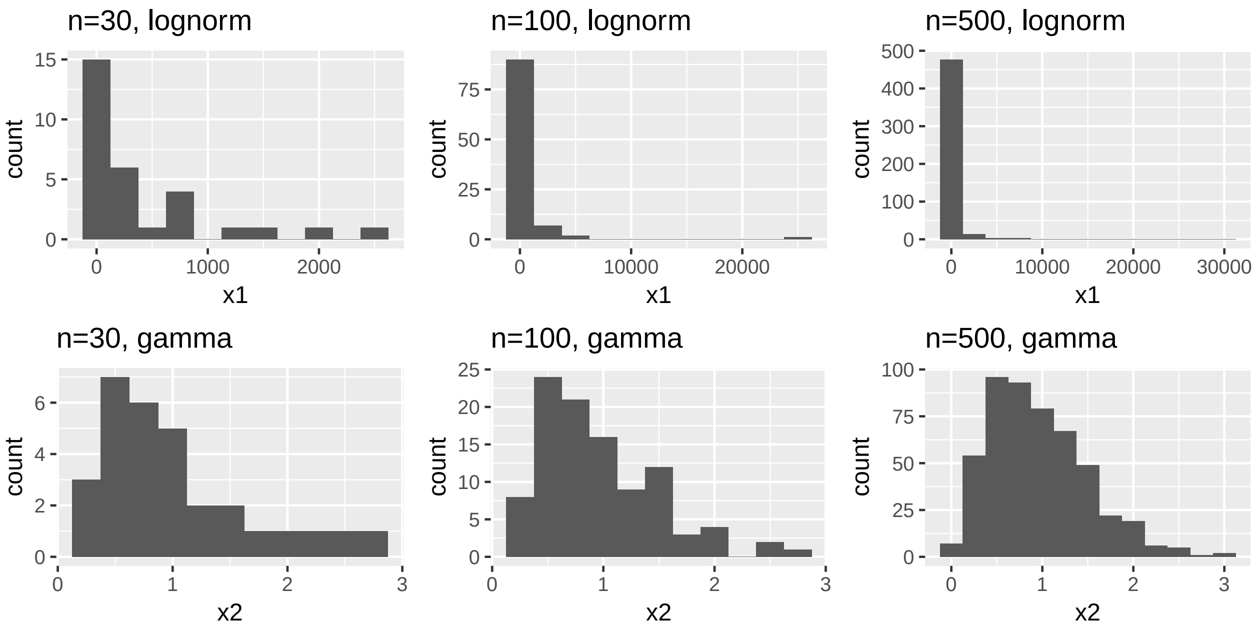
- Compute these probabilities for $X \sim N(3.3, 1.1)$
  - $P(X < 1.3)$ 0.0345182
  - $P(X > 1.9)$ 0.8984426
  - $P(1.8 < X < 2.2)$ 0.0723142
- Compute the quantile value (X) for $X \sim N(-10, 4)$ which matches these probabilities
  - $P(X < x) = 0.53$ -9.6989206
  - $P(X < x) = 0.12$ -14.6999472
  - $P(X < x) = 0.84$ -6.0221685
  - $P(X < x) = 1.2$ `Not possible`
- Compute the value of the density function for a $N(12, 5)$ corresponding to $X =$
  - 13.0 0.0782085
  - 4.0 0.0221842
  - 20.0 0.0221842
- Plot the density curves a
  - $Weibull(3, 1.5)$
  - $Weibull(2, 2)$
  - $Weibull(1, 1)$ on the same plot.



Question 1 (9pts)

a. (2pt) Simulate samples of size $n = 30$, 100, 500 from these distributions
   i. Lognormal(4, 2)
   ii. Gamma(3, 3)

```r
library(gridExtra)
set.seed(4)
df_30 <- data.frame(x1=rlnorm(30, 4, 2), x2=rgamma(30, 3, 3))
p1 <- ggplot(df_30, aes(x=x1)) + geom_histogram(binwidth=250) + ggtitle("n=30, lognorm")
p2 <- ggplot(df_30, aes(x=x2)) + geom_histogram(binwidth=0.25) + ggtitle("n=30, gamma")
df_100 <- data.frame(x1=rlnorm(100, 4, 2), x2=rgamma(100, 3, 3))
p3 <- ggplot(df_100, aes(x=x1)) + geom_histogram(binwidth=2500) + ggtitle("n=100, lognorm")
p4 <- ggplot(df_100, aes(x=x2)) + geom_histogram(binwidth=0.25) + ggtitle("n=100, gamma")
df_500 <- data.frame(x1=rlnorm(500, 4, 2), x2=rgamma(500, 3, 3))
p5 <- ggplot(df_500, aes(x=x1)) + geom_histogram(binwidth=2500) + ggtitle("n=500, lognorm")
p6 <- ggplot(df_500, aes(x=x2)) + geom_histogram(binwidth=0.25) + ggtitle("n=500, gamma")
grid.arrange(p1, p3, p5, p2, p4, p6, ncol=3)
```



b. (2pt) Do an internet search to find an example of where a lognormal distribution, and a gamma distribution might be used.

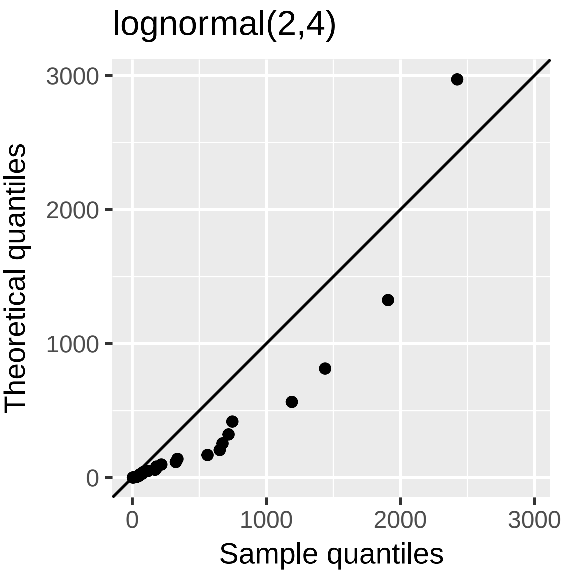
```
Lognormal: (http://www.statisticshowto.com/lognormal-distribution/)
- Milk production by cows.
- Lives of industrial units with failure modes that are characterized by fatigue-stress.
- Amounts of rainfall.
- Size distributions of rainfall droplets.
- The volume of gas in a petroleum reserve.
gamma: (https://en.wikipedia.org/wiki/Gamma_distribution)
 the waiting time until death
```

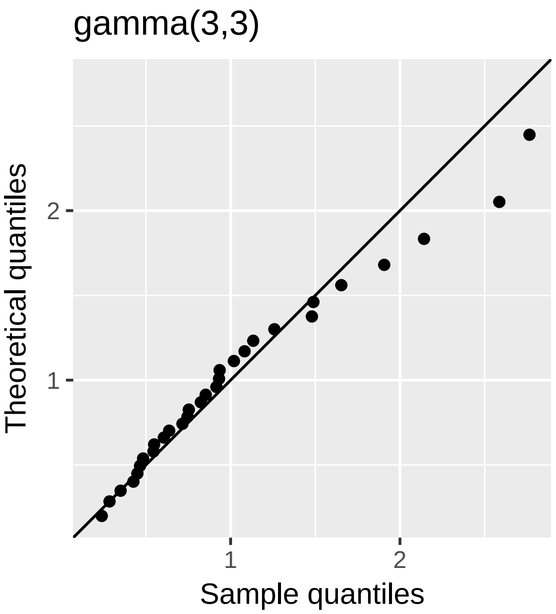
```
Be sure to provide the reference link for your information.
```

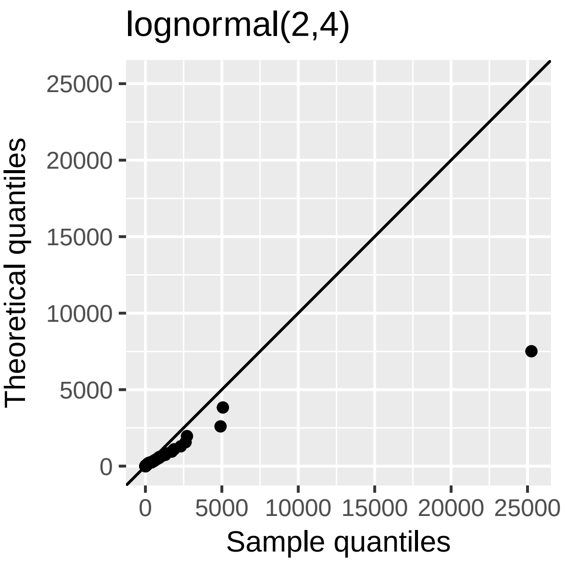
c. (5pt) Make a QQ-plot of each these samples. Explain how closely the samples, of different sizes, appears to match the theoretical distribution.

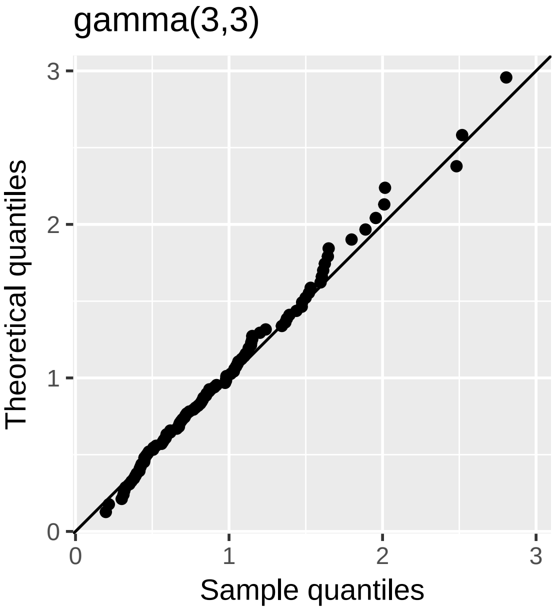
```r
n <- 30
df_30$x1q = qlnorm(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 4, 2)
df_30$x2q = qgamma(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 3, 3)
lims1 <- c(min(min(df_30$x1), min(df_30$x1q)), max(max(df_30$x1), max(df_30$x1q)))
lims2 <- c(min(min(df_30$x2), min(df_30$x2q)), max(max(df_30$x2), max(df_30$x2q)))
p1 <- ggplot(df_30, aes(x=sort(x1), y=x1q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims1) + ylim(lims1) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("lognormal(2,4)")
p2 <- ggplot(df_30, aes(x=sort(x2), y=x2q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims2) + ylim(lims2) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("gamma(3,3)")
```

```r
grid.arrange(p1, p2, ncol=2)
n <- 100
df_100$x1q = qlnorm(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 4, 2)
df_100$x2q = qgamma(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 3, 3)
lims1 <- c(min(min(df_100$x1), min(df_100$x1q)), max(max(df_100$x1), max(df_100$x1q)))
lims2 <- c(min(min(df_100$x2), min(df_100$x2q)), max(max(df_100$x2), max(df_100$x2q)))
p1 <- ggplot(df_100, aes(x=sort(x1), y=x1q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims1) + ylim(lims1) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("lognormal(2,4)")
p2 <- ggplot(df_100, aes(x=sort(x2), y=x2q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims2) + ylim(lims2) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("gamma(3,3)")
grid.arrange(p1, p2, ncol=2)
n <- 500
df_500$x1q = qlnorm(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 4, 2)
df_500$x2q = qgamma(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
                       (n + 0.365),0.5^(1/n)), 3, 3)
lims1 <- c(min(min(df_500$x1), min(df_500$x1q)), max(max(df_500$x1), max(df_500$x1q)))
lims2 <- c(min(min(df_500$x2), min(df_500$x2q)), max(max(df_500$x2), max(df_500$x2q)))
p1 <- ggplot(df_500, aes(x=sort(x1), y=x1q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims1) + ylim(lims1) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("lognormal(2,4)")
p2 <- ggplot(df_500, aes(x=sort(x2), y=x2q)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + coord_equal() +
  xlim(lims2) + ylim(lims2) +
  xlab("Sample quantiles") + ylab("Theoretical quantiles") +
  ggtitle("gamma(3,3)")
grid.arrange(p1, p2, ncol=2)
```


lognormal(2,4)
Theoretical quantiles
Sample quantiles
0
1000
2000
3000
0
1000
2000
3000


gamma(3,3)
Theoretical quantiles
Sample quantiles
1
2
1
2


lognormal(2,4)
Theoretical quantiles
Sample quantiles
0
5000
10000
15000
20000
25000
0
5000
10000
15000
20000
25000


gamma(3,3)
Theoretical quantiles
Sample quantiles
0
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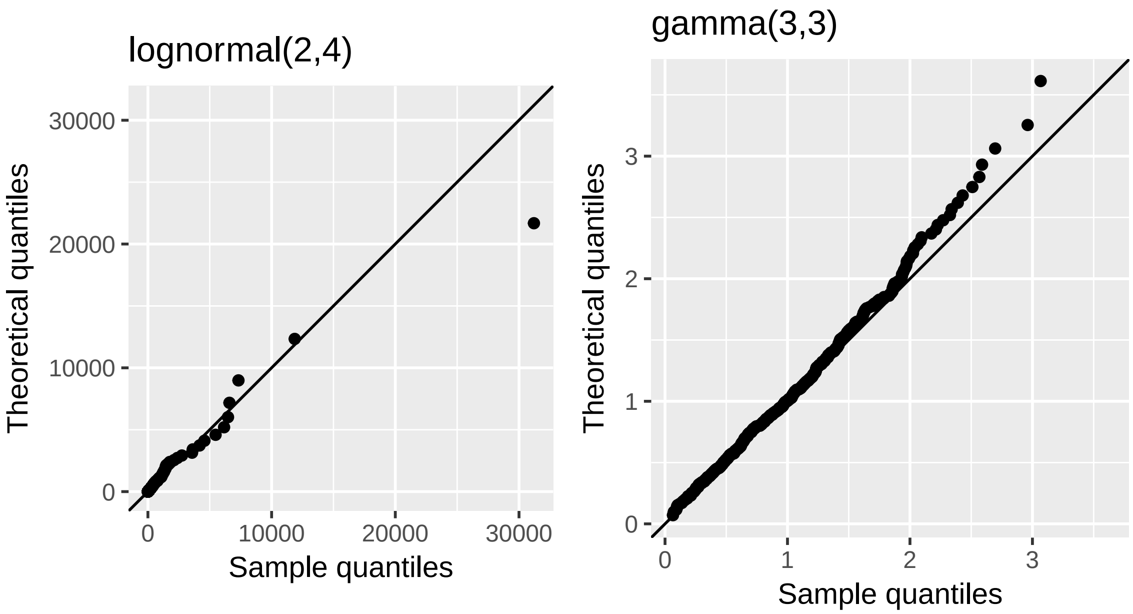


`With larger sample sizes the points should lie more closely on the guide line. For the most part this i`

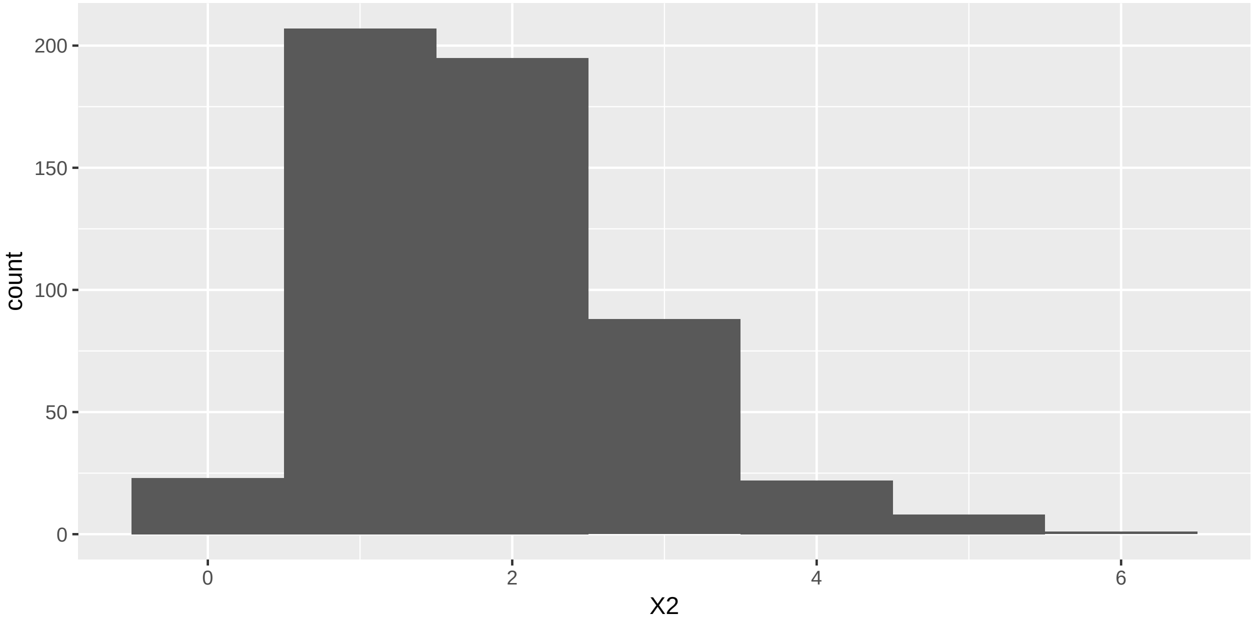
Question 2 (12pts)

Using this code, generate a sample of size $n = 544$ from a $Gamma(3.2, 1.7)$ distribution.

```
set.seed(123)
X2 <- rgamma(n=544, 3.2, 1.7)
```

a. (2pt) Plot the sample, using a histogram, describe the shape of the distribution. `unimodal, slightly right-skewed`

```
ggplot(data.frame(X2), aes(x=X2)) + geom_histogram(binwidth=1)
```



b. (1pt) What parameters of the gamma distribution were used to simulate the sample? ($\alpha = 3.2, \beta = 1.7$)

c. (1pt) If we are to use maximum likelihood distribution what values would we expect to get as the parameter estimates? `(3.2, 1.7)`

d. (2pt) Write a function to compute the likelihood function.

```
nmle <- function(x, a, b) {
  f <- prod(dgamma(x, a, b))
  return(f)
}
```

e. (3pt) Plot the likelihood function for a range of values of α, β that shows the maximum likelihood estimates for each parameter.

```
a <- seq(2.5, 4.2, 0.05)
b <- seq(1.5, 2.5, 0.05)
g <- expand.grid(x=a, y=b)
g$f <- 0
for (i in 1:nrow(g)) {
  cat(i,"\n")
  g$f[i] <- nmle(X2, g$x[i], g$y[i])
}
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ggplot(g, aes(x=x, y=y, fill=f)) + geom_tile() + xlab(expression(alpha)) + ylab(expression(beta)) + ther
  scale_fill_continuous("L") +
  theme(aspect.ratio=1)
```
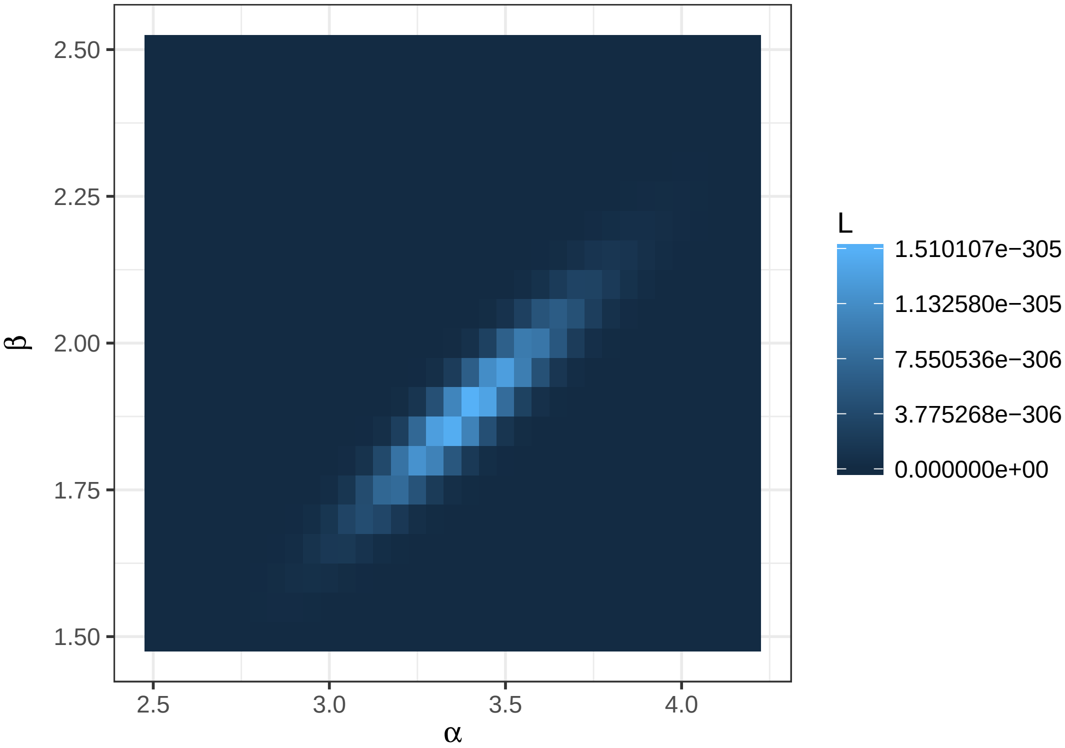



```
g[which.max(g$f),]
#       x   y            f
# 299 3.4 1.9 1.510107e-305
```

f. (3pt) Look up the function `fitdistr` from the `MASS` library. Explain what this does. Use it to find the MLE estimates for α, β. How do these compare with the values you read off your plot? `The values from the plot are very similar.`

```
library(MASS)
fitdistr(X2, "gamma")
#      shape       rate
#   3.3879099   1.8832870
#  (0.1961500) (0.1175305)
```

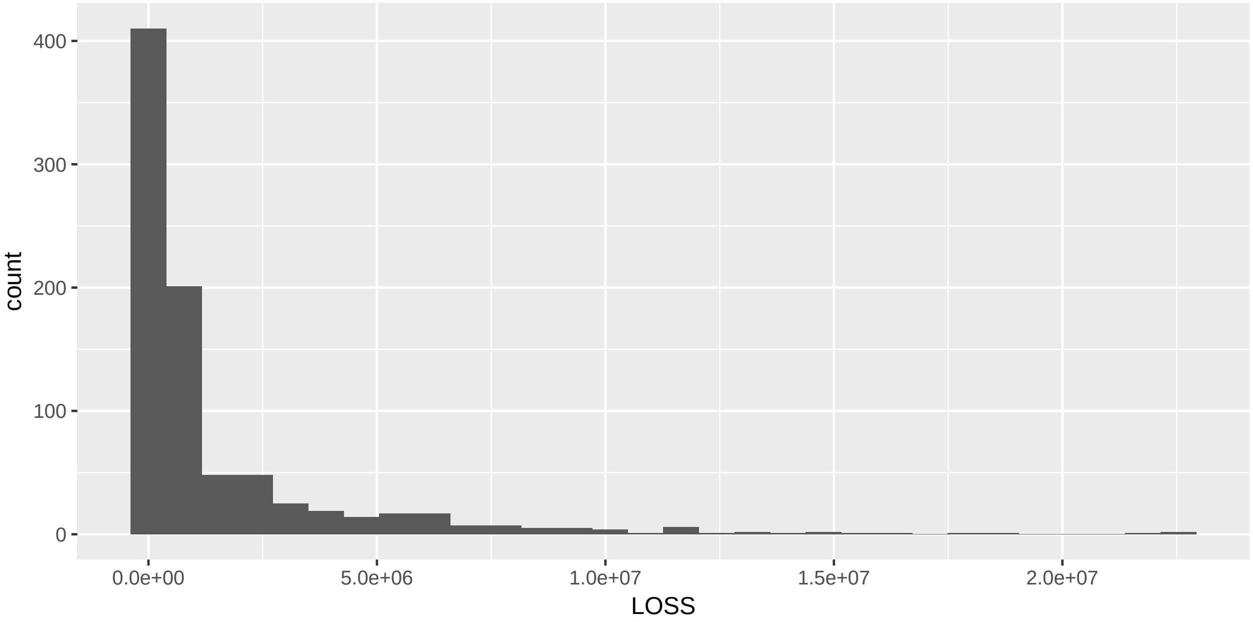
Question 3 (9pts)

Take a look at the data set `usworkcomp` from the `CASdatasets` library. Read the documentation about this data on http://cas.uqam.ca/pub/R/web/CASdatasets-manual.pdf.

A copy of the data is provided with the lab, in case the CASdatasets are not all available.

a. (2pt) Make a histogram of the `LOSS`. Describe the shape. `Heavily right-skewed, unimodal`

```
ggplot(usworkcomp, aes(x=LOSS)) + geom_histogram()
```

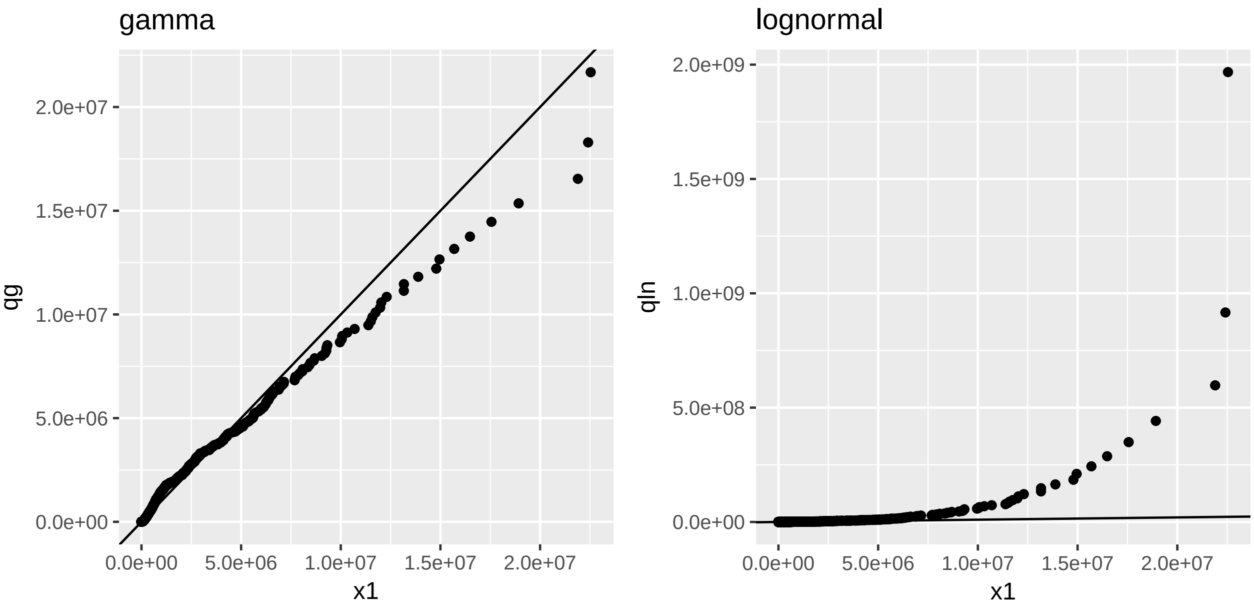


b. (3pt) Fit both a gamma and lognormal distribution to the sample, i.e. find the MLEs.

```
fitdistr((usworkcomp$LOSS+100)/100000, "gamma")
#       shape         rate
#   0.367774667   0.023499352
#  (0.014346994) (0.001614735)
fitdistr((usworkcomp$LOSS+100)/100000, "lognormal")
#     meanlog       sdlog
#   0.93691677   2.84185608
#  (0.09764733) (0.06904709)
```

c. (2pt) Produce a QQ-plot for each of the distributions.

```
n <- nrow(usworkcomp)
df <- data.frame(x1=sort(usworkcomp$LOSS))
df$qg = (qgamma(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
     (n + 0.365),0.5^(1/n)), 0.367774667, 0.023499352))*100000-100
df$qln = (qlnorm(c(1 - 0.5^(1/n), (2:(n-1) - 0.3175) /
     (n + 0.365),0.5^(1/n)), 0.93691677, 2.84185608))*100000-100
p1 <- ggplot(df, aes(x=x1, y=qg)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + theme(aspect.ratio=1) +
  ggtitle("gamma")
p2 <- ggplot(df, aes(x=x1, y=qln)) +
  geom_abline(intercept=0, slope=1) +
  geom_point() + theme(aspect.ratio=1) +
  ggtitle("lognormal")
grid.arrange(p1, p2, ncol=2)
```



d. (2pt) Which is the better fit to the sample? `Gamma. It is fairly close, except for high values.`

TURN IN

- Your `.Rmd` file
- Your html file that results from knitting the Rmd.
- Make sure your group members are listed as authors, one person per group will turn in the report